Amendments to the Claims

This listing of claims replaces all prior versions and listings of claims in the application.

Listing of Claims

1. to 46. (cancelled)

47. (currently amended) A method of diagnosing a non-central nervous system (non-CNS) disorder in a subject, the method comprising:

detecting expression of one or more genes in a ~~CNS~~ sample ~~of the subject, wherein the CNS sample comprises~~ comprising a cell from the brain of the subject, a cell from the spinal cord of the subject, or cerebrospinal fluid (CSF), and the gene expression data corresponds to the presence or level of ~~the~~ a protein in the sample;

generating gene expression data from the detected gene expression;

obtaining a reference gene expression profile for a specific non-CNS disorders; and

comparing the gene expression data with the reference gene expression profile, wherein a match of the ~~CNS~~ sample gene expression data to the reference gene expression profile indicates the subject has or will develop the non-CNS disorder.

48. (currently amended) The method of claim 47, wherein the ~~CNS~~ sample comprises cerebrospinal fluid (CSF), and the gene expression data corresponds to a protein in the CSF.

49. (cancelled)

50. (currently amended) The method of claim 47, wherein the protein is selected from the group consisting of a hormone, a growth factor, an immune system component, ~~and~~ a cytokine, and a non-secreted cellular protein.

51. (canceled)

52. (previously presented) The method of claim 47, wherein the gene encodes a gene product selected from the group consisting of hepatocyte growth factor (HGF), apherin A3, chemokine (C-C motif) ligand 4, growth differentiation factor-9b (GDF-9b); bone morphogenetic protein 15 (BMP 15), neuroblastoma suppressor of tumorigenicity 1, melanocyte proliferating gene 1, and fibroblast growth factor 22 (FGF 22).

53. (currently amended) The method of claim 47, wherein the ~~CNS~~ sample is a sample of one or more cells from the brain, and the gene expression data corresponds to a nucleic acid molecule or protein in the sample.

54. (previously presented) The method of claim 53, wherein the brain cells are selected from the group consisting of cells from the hypothalamus, the midbrain, the prefrontal cortex, and the striatum.

55. (previously presented) The method of claim 53, wherein the nucleic acid molecule comprises mRNA corresponding to the gene.

56. (previously presented) The method of claim 47, wherein two or more reference gene expression profiles are used, each specific for a different non-CNS disorder.

57. (previously presented) The method of claim 47, wherein the non-CNS disorder is selected from the group consisting of cancer, rheumatoid arthritis, asthma, diabetes, and obesity.

58. (previously presented) The method of claim 47, wherein the non-CNS disorder is cancer.

59. (previously presented) The method of claim 47, wherein the non-CNS disorder is a solid tumor less than 0.5 cm in diameter.

60. (currently amended) The method of claim 47, wherein the gene expression data comprises data for a plurality of genes in the ~~CNS~~ sample, and comprises a gene expression profile.

61. (currently amended) The method of claim 47, further comprising

obtaining a control gene expression profile corresponding to one or more healthy subjects; and

comparing the gene expression data with the control gene expression profile, wherein a match of the ~~CNS~~ sample gene expression data to the control gene expression profile indicates the subject does not have and will not likely develop the non-CNS disorder.

62. (previously presented) The method of claim 47, wherein the gene expression is detected using a microarray assay.

63. (previously presented) The method of claim 47, wherein the subject is a human.

64. (previously presented) The method of claim 63, wherein the subject has a family history of the disorder.

65. (previously presented) The method of claim 47, wherein the subject lacks a clinical sign of a disorder as evaluated by imaging analysis.

66. (previously presented) The method of claim 47, wherein the subject is a carrier of a gene associated with an increased risk of developing the disorder.

67. (previously presented) The method of claim 66, wherein the subject is a carrier of the BRCA1, BRCA2, hMSH2, hMLH1, or hMSH6 gene.

68-85. (cancelled)

86. (previously presented) The method of claim 47, wherein the gene encodes a gene product selected from the group consisting of:

For Breast Cancer: Nedd8 (FIG. 29-1), Col4a3bp (FIG. 29-2), Bgn (FIG. 29-4), Sox5 (FIG. 29-5), Slc38a4 (FIG. 32-1), Tom1 (FIG. 32-2), Calr (FIG. 32-4), Itgae (FIG. 32-5), Ttrap (FIG. 35-1), Pex11b (FIG. 35-2), Sema7a (FIG. 35-4), and Stam2 (FIG. 35-5);

For Colon Cancer: Nmb (FIG. 30-1), Ryr2 (FIG. 30-2), Trfr (FIG. 30-4), Mfap5 (FIG. 30-5), Prrg2 (FIG. 33-1), Faim (FIG. 33-2), Mgrn1 (FIG. 33-4), Stch (FIG. 33-5), Lhb (FIG. 36-1), Prm3 (FIG. 36-2), Crry (FIG. 36-4), and Timp4 (FIG. 36-5);

For Lung cancer: Nmb (FIG. 31-1), Pcdh8 (FIG. 31-2), Rock2 (FIG. 31-4), Angptl3 (FIG. 31-5), Sqstm1 (FIG. 34-1), Kcnip2 (FIG. 34-2), Oxt (FIG. 34-4), Myh4 (FIG. 34-5), Enc1 (FIG. 37-1), Gsg1 (FIG. 37-2), Srr (FIG. 37-4), and Ndph (FIG. 37-5);

For Arthritis: Bcl2l (FIG. 51A), P2rx1 (FIG. 51B), Pafah1b1 (FIG. 51B), Kcna3 (FIG. 51C), Taf1b (FIG. 51C), Slc38a3 (FIG. 51D), Hprt (FIG. 52A), C1d (FIG. 52B), Car11 (FIG. 52D), Dusp3 (FIG. 52D), Gabrr2 (FIG. 53C), and Aatk (FIG. 53D); and

For Asthma: Rasa3 (FIG. 55B), Tnk2 (FIG. 55B), H28 (FIG. 55C), Diap2 (FIG. 55C), Lgals6 (FIG. 56A), Reck (FIG. 56A), Whrn (FIG. 56A), Stk22s1 (FIG. 56B), CD47 (FIG. 57A), Jund1 (FIG. 57A), Cstb (FIG. 57B), and Desrt (FIG. 57B).

87. (new) The method of claim 47, wherein the sample consists essentially of a cell from the brain of the subject, a cell from the spinal cord of the subject, or cerebrospinal fluid (CSF)